PHYLOGENETIC RELATIONSHIPS AMONG MAHSEERS (CYPRINIDAE) IN MALAYSIA INFERRED FROM SEQUENCING OF A CYTOCHROME C OXIDASE I (COI) MITOCHONDRIAL DNA (mtDNA) SEGMENT

[1, 2]Yuzine B. Esa, [3]Kamarul Rahim Kamaruddin, [4]Jeffrine Rovie R. Japning, [1]Khairul Adha A. Rahim, [2]Siti Khalijah Daud, [2]Siti Shapor Siraj and [2]Tan Soon Guan

[1] Faculty of Resource Science and Technology, Universiti Malaysia Sarawak
[2] Department of Biology, Faculty of Science, Universiti Putra Malaysia, Selangor,
[3] Department of Biotechnology, Kulliyyah of Science,
International Islamic University Malaysia (IIUM) Kuala Lumpur
[4] Institute of Biodiversity, Pahang,

The present study examines the phylogenetic relationships among *Tor douronensis, T. tambra, T. tambroides* of the genus *Tor* and *Neolissochilus stracheyi* representing the genus Neolissochilus, by using the partial sequencing of the mitochondrial DNA cytochrome c oxidase I (COI) gene. Samples were collected from various rivers throughout Sarawak, Sabah and Peninsular Malaysia. The phylogenetic analysis obtained by using the Neighbour Joining (NJ) and Maximum Parsimony (MP) procedures supported the monophyletic status among the three mahseers, except between *T. tambroides* and *T. tambra*. The high genetic divergence separating *T. douronensis* and *T. tambroides* or *T. tambra* confirmed their status as distinct species. Likewise, the high genetic divergence separating the *N. stracheyi* lineage from the Tor lineages (7.3-11.0%) also supported its recent reclassification from the genus *Tor* into the genus *Neolissochilus*. The identical haplotypes found between all the *T. tambra* sequences with most of the *T. tambroides* sequences indicated a very close genetic relationship between them. Similarly, the close genetic relationships (0-0.4%) found between *T. tambroides* samples from Peninsular Malaysia (kelah fish) and those from Sarawak (empurau fish) supported their taxonomic status as belonging to the same species. Phylogenetic analysis also revealed that the *T. douronensis* mtDNA consisted of three highly distinct lineages (Sabah, northern and southern Sarawak), consistent with their geographical locations. However, our phylogenetic analysis did not find any *T. douronensis* group to be genetically more similar to *T. tambroides* (6.3-9.2%). Overall, the present study managed to provide useful insights into the phylogeny and taxonomy of the mahseers in Malaysia.